PCT/AU98/00795

WO 99/15647

FIGURE 1A

ATTCCTCTTCATAATGCATGCTCTTTTGGTCATGCTGAAGTAGTCAATCTCCTTTTGCGACATGGTGCAG $$ I $$ P $$ L $$ H $$ A $$ C $$ S $$ F $$ G $$ H $$ A $$ E $$ V $$ N $$ L $$ L $$ R $$ H $$ G $$ A	70
ACCCCAATGCTCGAGATAATTGGAATTATACTCCTCTCCATGAAGCTGCAATTAA λ GGAAAGATTGATGT DPNARDN WNYTPLHEAAIKGKIDV	140
TTGCATTGTGCTGTTACAGCATGGAGCTGAGCCAACCATCCGAAATACAGATGGAAGGACAGCATTGGAT C I V L L Q H G A E P T I R N T D G R T A L D	210
TTAGCAGATCCATCTGCCAAAGCAGTGCTTACTGGTGAATATAAGAAAGA	280
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	350
CAGAAAGTCAACTCCATTACATTTGGCAGCAGGATATAACAGAGTAAAGATTGTACAGCTGTTACTGCAA R K S T P L H L A A G Y N R V K I V Q L L L Q	420
CATGGACGTGATGTCCATGCTAAAGATAAAGGTGATCTGGTACCATTACACAATGCCTGTTCTTATGGTC H G R D V H A K D K G D L V P L H N A C S Y G	490
ATTATGAAGTAACTGAACTTTTGGTCAAGCATGGTGGCTGTGTAAATGCAATGGACTTGTGGCAATTCAC H Y E V T E L L V K H G G C V N A M D L W Q F T	560
TCCTCTTCATGAGGCAGCTTCTAAGAACAGGGTTGAAGTATGTTCTCTTCTCTTAAGTTATGGTGCAGAC PLHEAASKNRVEVCSLLLSYGAD	630
CCAACACTGCTCAATTGTAAGAATAAAAGTGCTATAGACTTGGCTCCCACACCACAGTTAAAAGAAAG	700
TAGCATATGAATTTAAAGGCCACTCGTTGCTGCAAGCTGCACGAGAAGCTGATGTTACTCGAATCAAAAA LAYEFKGHSLLQAAREADVTRIKK	770
ACATCTCTCTGGAAATGGTGAATTTCAAGCATCCTCAAACACATGAAACAGCATTGCATTGTGCTGCT H L S L E M V N F K H P Q $\underline{\text{T}}$ H E $\underline{\text{T}}$ A L H C A $\underline{\text{A}}$	840
GCATCTCCATATCCCAAAAGAAAGCAAATATGTGAACTGTTGCTAAGAAAAGGAGCAAACATCAATGAAA A S P Y P K R K Q I C E L L R K G A N I N E	910
AGACTAAAGAATTCTTGACTCCTCTGCACGTGGCATCTGAGAAAGCTCATAATGATGTTGTTGAAGTAGT K T K E F L T P L H V A S E K A H N D V V E V V	980
GGTGAAACATGAAGCAAAGGTTAATGCTCTGGATAATCTTGGTCAGACTTCTCTACACAGAGCTGCATAT ${f V}$ K H E A K V N A L D N L G Q T S L H R A A Y	1050
·	1120
GCTTTACTGCTTTACAGATGGGAAATGAAAATGTACAGCAACTCCTCCAAGAGGGTATCTCATTAGGTAAGGFFTALQMGNENVQQLLQEGISLGN	1190
	1260
ACTGTTCAGAGTGTCAACTGCAGAGACATTGAAGGGGCGTCAGTCTACACCACTTCATTTTGCAGCTGGGT T V Q S V N C R D I E G R Q S T P L H F A A G	1330
ATAACAGÄGTGTCCGTGGTGGAATATCTGCTACAGCATGGAGCTGATGTGCATGCTAAAGATAAAGGAGG Y N R V S V V E Y L L Q H G A D V H A K D K ${\sf G}$ G	1400
CCTTGTACCTTTGCACAATGCATGTTCTTACGGACATTATGAAGTTGCAGAACTTCTTGTTAAACATGGA LVPLHNACSYGHYEVAELLVKHG	1470
GCAGTAGTTAATGTAGCTGATTTATGGAAATTTACACCTTTACATGAAGCAGCAGCAAAAGGAAAATATG A V V N V A D L W K F T P L H E A A A K G K Y	1540
AAATTTGCAAACTTCTGCTCCAGCATGGTGCAGACCCTACAAAAAAAA	1610

1/4

WO 99/15647

PCT/AU98/00795

FIGURE 1B	2/4		
GGATCTTGTTAAAGATGGAGATAC	AGATATTCAAGATCTGCTTAGGGGAGAT DIQDLLRGD	GCAGCTTTGCTAGATGCT AA;LLDA	1680
GCCAAGAAGGGTTGTTTAGCCAGA A K K G C L A R	$egin{array}{lll} ext{GTGAAGAAGTTGTCTTCTCCTGATAATG} & V & K & L & S & P & D & N \end{array}$	TAAATTGCCGCGATACCC V N C R D T	1750
AAGGCAGACATTCAACACCTTTAC	CATTTAGCAGCTGGTTATAATAATTTAGA H L A A G Y N N L E	AGTTGCAGAGTATTTGTT V A E Y L L	1820
ACAACACGGAGCTGATGTGAATGC	CCCAAGACAAAGGAGGACTTATTCCTTTA A Q D K G G L I P L	CATAATGCAGCATCTTAC H N A A S Y	1890
GGGCATGTAGATGTAGCAGCTCTA	ACTAATAAAGTATAATGCATCTCTAATG L I K Y N A S L N	CCACGGACAAATGGGCTT A T D K W A	1960
TCACACCTTTGCACGAAGCAGCCCF T P L H E A A	CANAAGGGACGANCACAGCTTTGTGCTTT Q K G R T Q L C A I	GTTGCTAGCCCATGGAGC	2030
TGACCCGACTCTTAAAAATCAGG	AAGGACAAACACCTTTAGATTTAGTTTCA E G Q T P L D L V S	AGCAGATGATGTCAGCGCT A D D V S A	2100
CTTCTGACAGCAGCCATGCCCCCC	ATCTGCTCTGCCCTCTTGTTACAAGCCTC S A L P S C Y K P	CAAGTGCTCAATGGTGTGA Q V L N G V	2170
GAAGCCCAGGAGCCACTGCAGATC	GCTCTCTCTTCAGGTCCATCTAGCCCATC	CAAGCCTTTCTGCAGCCAG S S L S A A S	2240
CAGTCTTGACAACTTATCTGGGA S L D N L S G	GTTTTTCAGAACTGTCTTCAGTAGTTAG S F S E L S S V V S	TTCAAGTGGAACAGAGGT S S G T E G	2310
GCTTCCAGTTTGGAGAAAAAGGA A S S L E K K E	GGTTCCAGGAGTAGATTTTAGCATAACTC V P G V D F S I T	CAATTCGTAAGGAATCTTG Q F V R N L	2380
GACTTGAGCACCTAATGGATATA G L E H L M D I	TTTGAGAGAGAACAGATCACTTTGGATG FEREQITLD'	TATTAGTTGAGATGGGGCA V L V E M G H	2450
CAAGGAGCTGAAGGAGATTGGAA K E L K E I G	TCAATGCTTATGGACATAGGCACAAACT I N A Y G H R H K L	AATTAAAGGAGTCGAGAGA I K G V E R	2520
CTTATCTCCGGACAACAAGGTCT L I S G Q Q G L	TAACCCATATTTAACTTTGAACACCTCT NPYLTLNTS	GGTAGTGGAACAATTCTTA G S G T I L	2590
TAGATCTGTCTCCTGATGATAAA	GAGTTTCAGTCTGTGGAGGAAGAGATGC E F Q S V E E E M	AAAGTACAGTTCGAGAGCA Q S T V R E H	2660
CAGAGATGGAGGTCATGCAGGTG R D G G H A G	GAATCTTCAACAGATACAATATTCTCAA G I F N R Y N I L K	GATTCAGAAGGTTTGTAAC I O K V C N	2730
AAGAAACTATGGGAAAGATACAC K K L W E R Y T	TCACCGGAGAAAAGAAGTTTCTGAAGAA HRRKEVSEE	AACCACAACCATGCCAATG N H N H A N	2800
AACGAATGCTATTTCATGGGTCT E R M L F H G S	CCTTTTGTGAATGCAATTATCCACAAAG PFVNAIIHK	GCTTTGATGAAAGGCATGC G F D E R H A	2870
GTACATAGGTGGTATGTTTGGAC Y I G G M F G	GCTGGCATTTATTTTGCTGAAAACTCTTC A G I Y F A E N S S	CAAAAGCAATCAATATGTA K S N Q Y V	2940
TATGGAATTGGAGGAGGTÁCTG Y G I G G T (GGTGTCCAGTTCACAAAGACAGATCTTGI 5 C P V H K D R S C	TACATTTGCCACAGGCAGC Y I C H R Q	3010
TGCTCTTTTGCCGGGTAACCTTC	G K S F L Q F S A	ATGAAAATGGCACATTCTCC M K M A H S P	3080
TCCAGGTCATCACTCAGTCACTC	GGTAGGCCCAGTGTAAATGGCCTAGCATT G R P S V N G L A I	TAGCTGAATATGTTATTTAC LAEYVIY	3150
AGAGGAGANCAGGCTTATCCTG R G E Q A Y P	AGTATTTAATTACTTACCAGATTATGAG EYLITYQIMR	GCCTGAAGGTATGGTCGATG PEGMVD	3220
GATAAATAGTTATTTTAAGAAA G *	CTAATTCCACTGAACCTAAAATCATCAAA	AGCAGCAGTGGCCTCTACGT	3290

WO 99/15647

PCT/AU98/00795

FIGURE 1C

3/4.

TTTACTCCTTTGCTGAAAAAAATCATCTTGCCCACAGGCCTGTGGCAAAAGGATAAAATGTGAACGAA

360

GTTTAACATTCTGACTTGATAAAGCTTTAATAATGTACAG